

PATENT

Attorney Docket No. 14448-00017

IN THE UNITED STATES
PATENT AND TRADEMARK OFFICE

Application of: LAU, Lester F.

) CERTIFICATE OF MAILING BY "EXPRESS MAIL"

Continuation of:

) "Express Mail" Mailing Label Number

Serial No.: 09/142,569

) EL928527220 US

Filed: April 2, 1999

) Date of Deposit January 22, 2002

For: EXTRACELLULAR MATRIX
SIGNALLING MOLECULES

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Commissioner of Patents and Trademarks, Attention:
Assistant Commissioner for Patents, Washington, D.C.
20231

Group Art Unit: 1632

) Theresa A. Barnstable
(Typed or printed name of person mailing)

Examiner: J. T. Woitach

) *Theresa A. Barnstable*
(Signature of person mailing)

STATEMENT PURSUANT TO 37 C.F.R. § 1.821(g)

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

I hereby state that the content of the paper copy of the Sequence Listing, and the computer readable copy of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821-1.825, are the same and include no new matter.

Respectfully submitted,

By: *D.W.C.*

David W. Clough, Ph.D.
Registration No. 36,107
Attorney for Applicants

January 22, 2002

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02/15
[Signature]

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/053,753

DATE: 02/14/2002
TIME: 16:04:11

Input Set : A:\50013825_1.RTF
Output Set: N:\CRF3\02142002\J053753.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Lau, Lester F.
8 (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
10 (iii) NUMBER OF SEQUENCES: 17
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
14 (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
15 (C) CITY: Chicago
16 (D) STATE: Illinois
17 (E) COUNTRY: United States of America
18 (F) ZIP: 60606-6402
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US/10/053,753
C--> 28 (B) FILING DATE: 22-Jan-2002
29 (C) CLASSIFICATION:
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Clough, David W.
33 (B) REGISTRATION NUMBER: 36,107
34 (C) REFERENCE/DOCKET NUMBER: 28758/33766
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: 312/474-6300
38 (B) TELEFAX: 312/474-0448
39 (C) TELEX: 25-3856

41 (2) INFORMATION FOR SEQ ID NO: 1:

43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1480 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: single
47 (D) TOPOLOGY: linear
49 (ii) MOLECULE TYPE: protein
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 180..1316
55 (ix) FEATURE:
56 (A) NAME/KEY: misc_feature
57 (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Input Set : A:\50013825_1.RTF
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61	CGAGAGCGCC	CCAGAGAAGC	GCCTGCAATC	TCTGCCCTC	CTCCGCCAGC	ACCTCGAGAG	60
63	AAGGACACCC	GCCGCCCTCGG	CCCTCGCCTC	ACCGCACTCC	GGGCGCATTT	GATCCCGCTG	120
65	CTCGCCGGCT	TGTTGGTTCT	GTGTCGCCGC	GCTGCCCG	GTTCCCTCTG	CGGCCACA	179
67	ATG AGC TCC	AGC ACC TTC	AGG ACG CTC	GCT GTC	GCC GTC	ACC CTT CTC	227
68	Met Ser Ser	Ser Thr Phe	Arg Thr Leu Ala	Val Ala Val	Thr Leu Leu		
69	1	5	10	15			
71	CAC TTG ACC	AGA CTG GCG	CTC TCC ACC	TGC CCC	GCC GCC	TGC CAC TGC	275
72	His Leu Thr	Arg Leu Ala	Leu Ser Thr	Cys Pro Ala	Ala Cys His	Cys	
73	20	25	30				
75	CCT CTG GAG	GCA CCC AAG	TGC GCC CCG	GGA GTC	GGG TTG	GTC CGG GAC	323
76	Pro Leu Glu	Ala Pro Lys	Cys Ala Pro	Gly Val Gly	Leu Val Arg	Asp	
77	35	40	45				
79	GGC TGC GGC	TGC TGT AAG	GTC TGC GCT	AAA CAA CTC	AAC GAG GAC	TGC	371
80	Gly Cys Gly	Cys Cys Lys	Val Cys Ala	Lys Gln	Leu Asn Glu	Asp Cys	
81	50	55	60				
83	AGC AAA ACT	CAG CCC TGC	GAC CAC ACC	AAG GGG	TTG GAA	TGC AAT TTC	419
84	Ser Lys Thr	Gln Pro Cys	Asp His Thr	Lys Gly	Leu Glu Cys	Asn Phe	
85	65	70	75	80			
87	GGC GCC AGC	TCC ACC GCT	CTG AAA GGG	ATC TGC AGA	GCT CAG	TCA GAA	467
88	Gly Ala Ser	Ser Thr Ala	Leu Lys Gly	Ile Cys Arg	Ala Gln	Ser Glu	
89	85	90	95				
91	GGC AGA CCC	TGT GAA TAT	AAC TCC AGA	ATC TAC CAA	AAC GGG	GAA AGC	515
92	Gly Arg Pro	Cys Glu Tyr	Asn Ser Arg	Ile Tyr Gln	Asn Gly	Glu Ser	
93	100	105	110				
95	TTC CAG CCC AAC	TGT AAA CAC	CAG TGC ACA	TGT ATT GAT	GGC GGC	GTG	563
96	Phe Gln Pro	Asn Cys Lys	His Gln Cys	Thr Cys Ile	Asp Gly	Ala Val	
97	115	120	125				
99	GGC TGC ATT CCT	CTG TGT CCC	CAA GAA CTG	TCT CTC CCC	AAT CTG	GGC	611
100	Gly Cys Ile	Pro Leu Cys	Pro Gln Glu	Leu Ser	Leu Pro	Asn Leu Gly	
101	130	135	140				
103	TGT CCC AAC CCC	CGG CTG GTG	AAA GTC AGC	GGG CAG TGC	TGT GAA	GAG	659
104	Cys Pro Asn	Pro Arg Leu	Val Lys Val	Ser Gly	Gln Cys	Cys Glu	
105	145	150	155	160			
107	TGG GTT TGT GAT	GAA GAC AGC	ATT AAG GAC	TCC CTG GAC	GAC CAG	GAT	707
108	Trp Val Cys Asp	Glu Asp Ser	Ile Lys Asp	Ser Leu Asp	Asp Gln	Asp	
109	165	170	175				
111	GAC CTC CTC GGA	CTC GAT GCC	TCG GAG GTG	GAG TTA ACG	AGA AAC	AAT	755
112	Asp Leu Leu	Gly Leu Asp	Ala Ser Glu	Val Glu Leu	Thr Arg	Asn Asn	
113	180	185	190				
115	GAG TTA ATC	GCA ATT GGA	AAA GGC AGC	TCA CTG AAG	AGG CTT	CCT GTC	803
116	Glu Leu Ile	Ala Ile Gly	Lys Gly Ser	Ser Leu Lys	Arg Leu	Pro Val	
117	195	200	205				
119	TTT GGC ACC GAA	CCG CGA GTT	CTT TTC AAC	CCT CTG CAC	GCC CAT	GGC	851
120	Phe Gly Thr	Glu Pro Arg	Val Leu Phe	Asn Pro Leu	His Ala	His Gly	
121	210	215	220				
123	CAG AAA TGC ATC	GTT CAG ACC	ACG TCT TGG	TCC CAG TGC	TCC AAG	AGC	899
124	Gln Lys Cys Ile	Val Gln Thr	Ser Trp Ser	Gln Cys Ser	Lys Ser		
125	225	230	235	240			
127	TGC GGA ACT GGC	ATC TCC ACA CGA	GTT ACC AAT	GAC AAC CCA	GAG	TGC	947

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128	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys
129					245				250						255	
131	CGC	CTG	GTG	AAA	GAG	ACC	CGG	ATC	TGT	GAA	GTG	CGT	CCT	TGT	GGA	CAA
132	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	Gly	Gln
133					260				265						270	
135	CCA	GTG	TAC	AGC	AGC	CTA	AAA	AAG	GGC	AAG	AAA	TGC	AGC	AAG	ACC	AAG
136	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys	Thr	Lys
137					275				280						285	
139	AAA	TCC	CCA	GAA	CCA	GTC	AGA	TTT	ACT	TAT	GCA	GGA	TGC	TCC	AGT	GTC
140	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Ser	Ser	Val
141					290				295						300	
143	AAG	AAA	TAC	CGG	CCC	AAA	TAC	TGC	GGC	TCC	TGC	GTA	GAT	GGC	CGG	TGC
144	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys
145	305					310				315					320	
147	TGC	ACA	CCT	CTG	CAG	ACC	AGA	ACT	GTG	AAG	ATG	CGG	TTC	CGA	TGC	GAA
148	Cys	Thr	Pro	Leu	Gln	Thr	Arg	Thr	Val	Lys	Met	Arg	Phe	Arg	Cys	Glu
149						325				330					335	
151	GAT	GGA	GAG	ATG	TTT	TCC	AAG	AAT	GTC	ATG	ATG	ATC	CAG	TCC	TGC	AAA
152	Asp	Gly	Glu	Met	Phe	Ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser	Cys	Lys
153					340				345						350	
155	TGT	AAC	TAC	AAC	TGC	CCG	CAT	CCC	AAC	GAG	GCA	TCG	TTC	CGA	CTG	TAC
156	Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro	Asn	Glu	Ala	Ser	Phe	Arg	Leu	Tyr
157					355				360						365	
159	AGC	CTA	TTC	AAT	GAC	ATC	CAC	AAG	TTC	AGG	GAC	TAAGTGCCTC	CAGGGTTCCCT			1336
160	Ser	Leu	Phe	Asn	Asp	Ile	His	Lys	Phe	Arg	Asp					
161					370				375							
163	AGTGTGGGCT	GGACAGAGGA	GAAGCGCAAG	CATCATGGAG	ACGTGGGTGG	GC GGAGGATG										1396
165	AATGGTGCT	TGCTCATTCT	TGAGTAGCAT	TAGGGTATTT	CAAAACTGCC	AAGGGCTGA										1456
167	TGTGGACGGA	CAGCAGCGCA	GCCG													1480
169	(2)	INFORMATION FOR SEQ ID NO: 2:														
171	(i)	SEQUENCE CHARACTERISTICS:														
172		(A) LENGTH: 379 amino acids														
173		(B) TYPE: amino acid														
174		(D) TOPOLOGY: linear														
176	(ii)	MOLECULE TYPE: protein														
178	(ix)	FEATURE:														
179		(A) NAME/KEY: misc_feature														
180		(D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"														
182	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:														
184	Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu
185	1					5				10					15	
187	His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys
188						20				25					30	
190	Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp
191						35				40					45	
193	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys
194						50				55					60	
196	Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe
197						65				70					80	

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199 Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
200 85 90 95
202 Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
203 100 105 110
205 Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
206 115 120 125
208 Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
209 130 135 140
211 Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
212 145 150 155 160
214 Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
215 165 170 175
217 Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
218 180 185 190
220 Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
221 195 200 205
223 Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
224 210 215 220
226 Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
227 225 230 235 240
229 Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
230 245 250 255
232 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
233 260 265 270
235 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
236 275 280 285
238 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
239 290 295 300
241 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
242 305 310 315 320
244 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
245 325 330 335
247 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
248 340 345 350
250 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
251 355 360 365
253 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
254 370 375
256 (2) INFORMATION FOR SEQ ID NO: 3:
258 (i) SEQUENCE CHARACTERISTICS:
259 (A) LENGTH: 1418 base pairs
260 (B) TYPE: nucleic acid
261 (C) STRANDEDNESS: single
262 (D) TOPOLOGY: linear
264 (ii) MOLECULE TYPE: protein
266 (ix) FEATURE:
267 (A) NAME/KEY: CDS
268 (B) LOCATION: 124..1266
270 (ix) FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/053,753

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Input Set : A:\50013825_1.RTF
Output Set: N:\CRF3\02142002\J053753.raw

271 (A) NAME/KEY: misc_feature
 272 (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"
 274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 276 GGGCGGGCCC ACCCGCACAC CGCGCCGCCA CCCCGACCCC GCTGCGCACG GCCTGTCCGC 60
 278 TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC 120
 280 ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT 168
 281 Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
 282 1 5 10 15
 284 CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC 216
 285 Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
 286 20 25 30
 288 TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG 264
 289 Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
 290 35 40 45
 292 GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC 312
 293 Asp Gly Cys Gly Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
 294 50 55 60
 296 TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC 360
 297 Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
 298 65 70 75
 300 TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA 408
 301 Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
 302 80 85 90 95
 304 GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA 456
 305 Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
 306 100 105 110
 308 AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC 504
 309 Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
 310 115 120 125
 312 GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG 552
 313 Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
 314 130 135 140
 316 GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG 600
 317 Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu
 318 145 150 155
 320 GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG 648
 321 Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln
 322 160 165 170 175
 324 GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG 696
 325 Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu
 326 180 185 190
 328 TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG 744
 329 Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu
 330 195 200 205
 332 AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT 792
 333 Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro
 334 210 215 220
 336 TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC 840
 337 Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Ser Trp Ser Gln Cys

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/053,753

DATE: 02/14/2002
TIME: 16:04:12

Input Set : A:\50013825_1.RTF
Output Set: N:\CRF3\02142002\J053753.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:651 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:886 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:907 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:928 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:949 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:970 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17